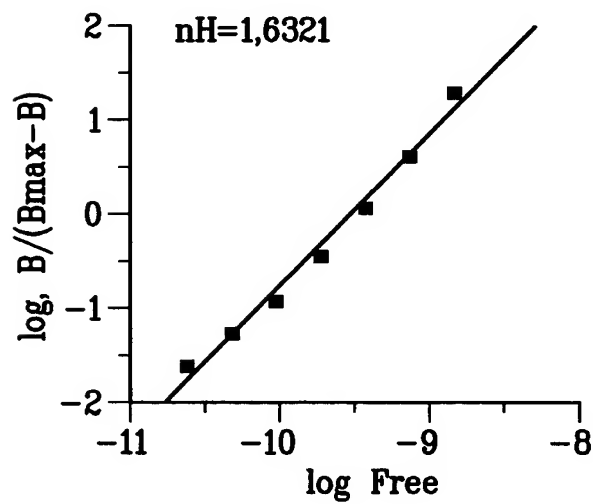
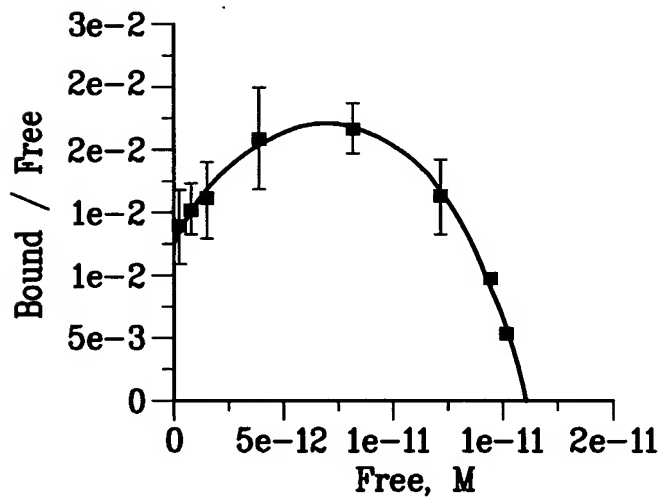
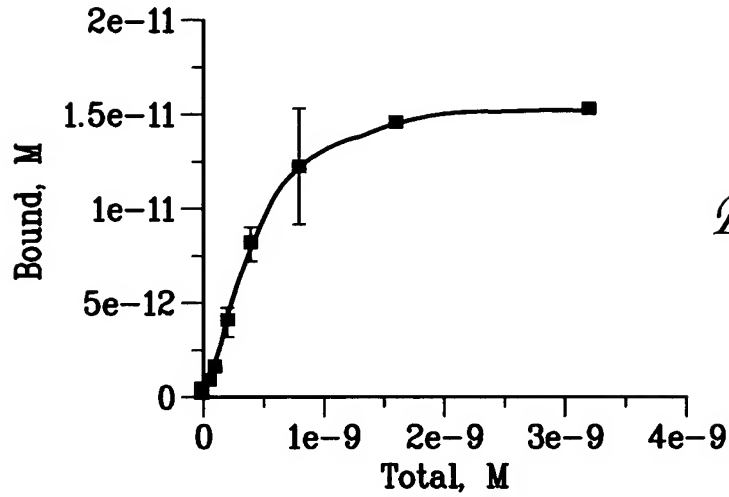


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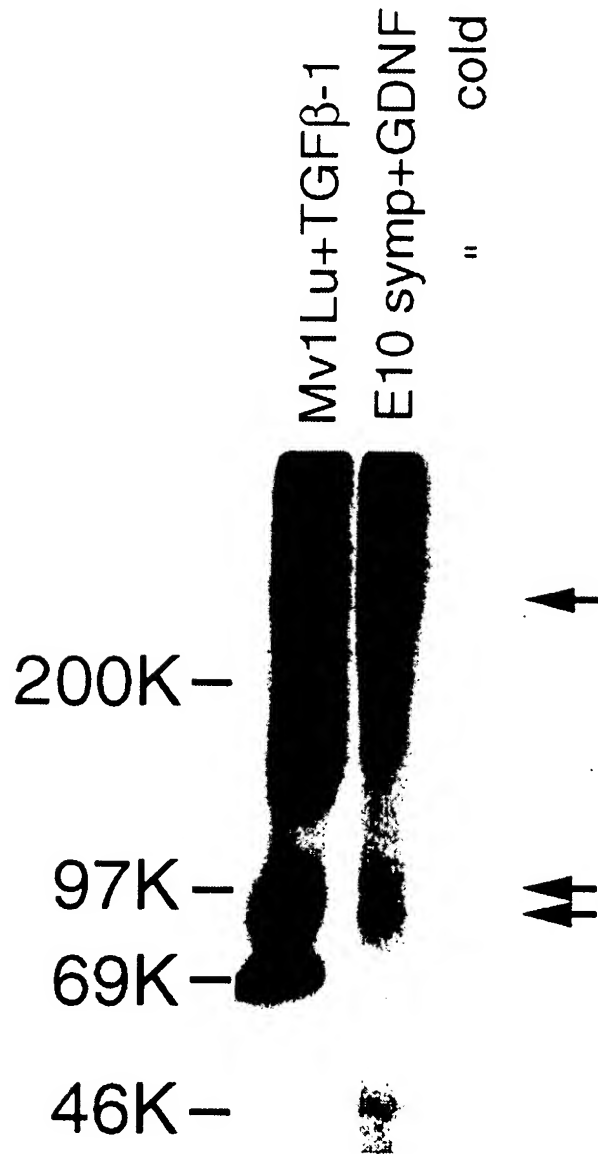


FIG. 2

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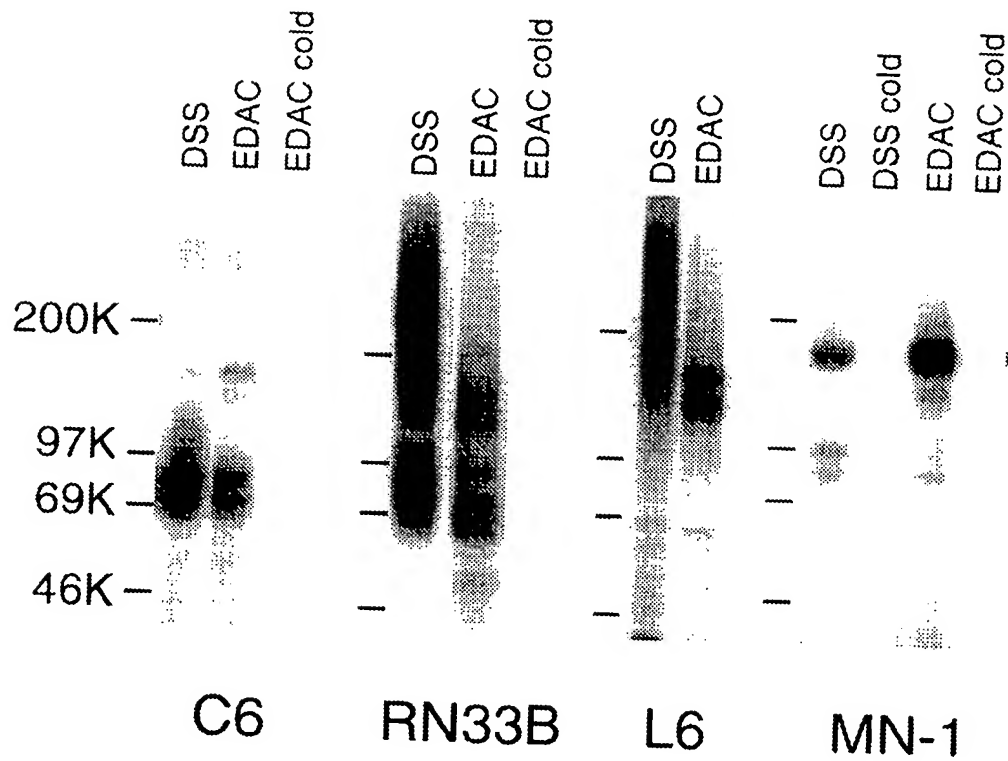


FIG. 3

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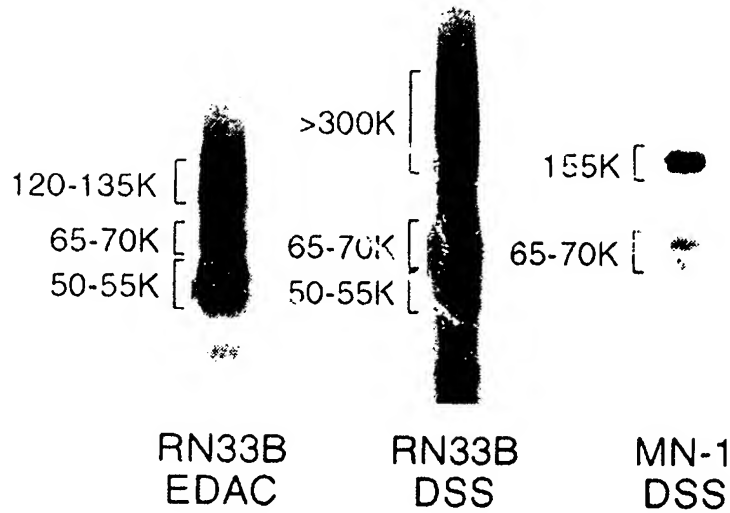


FIG. 4A

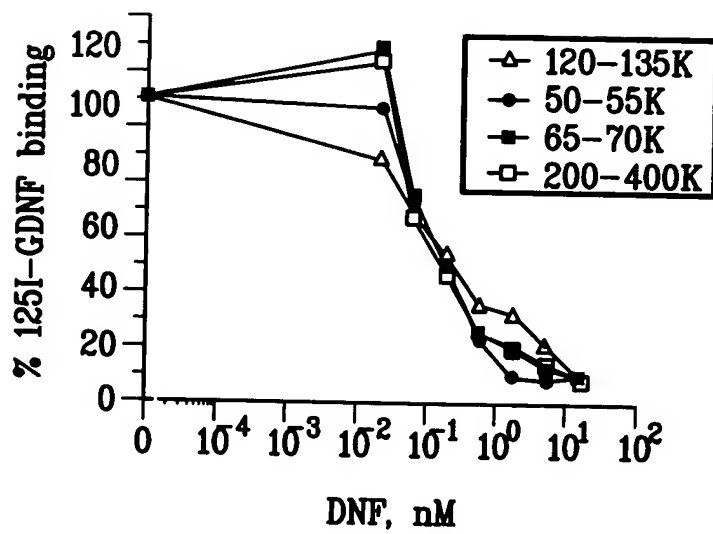


FIG. 4B

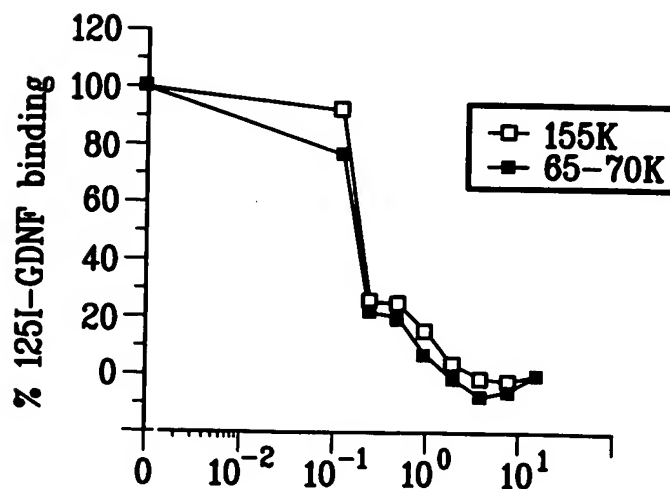
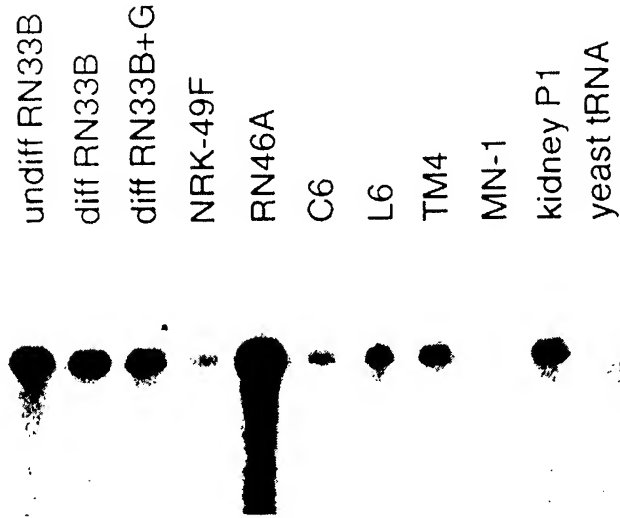
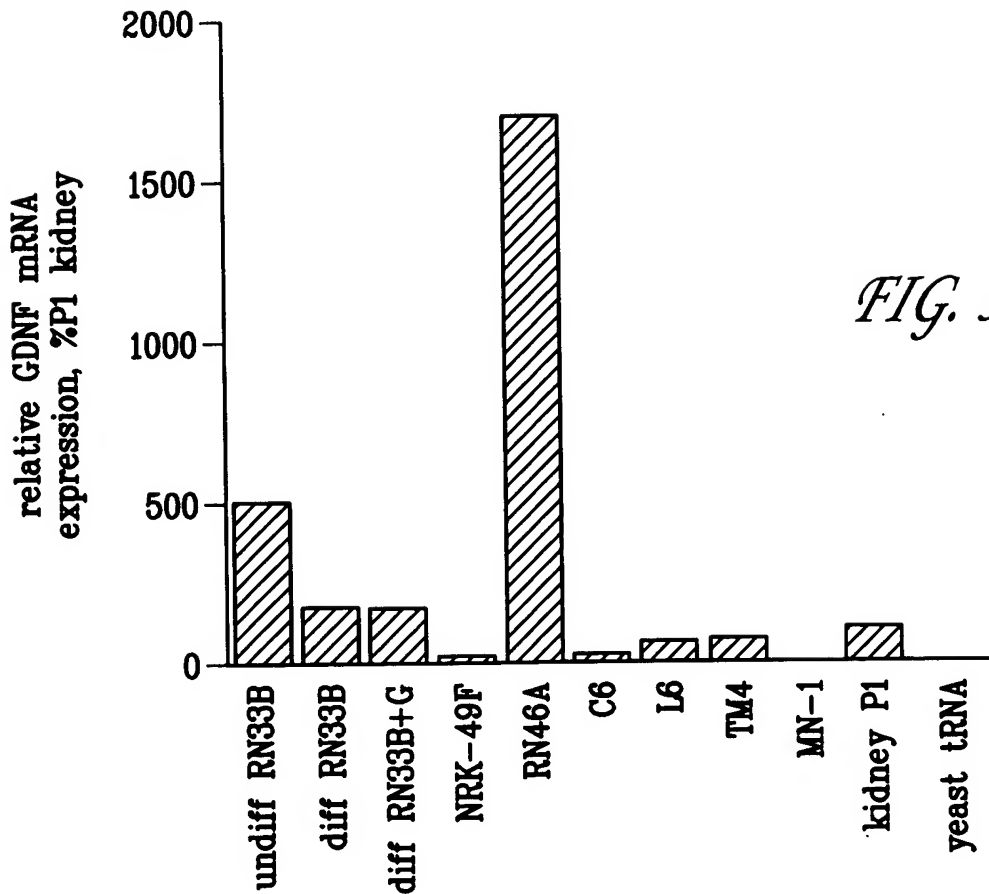


FIG. 4C

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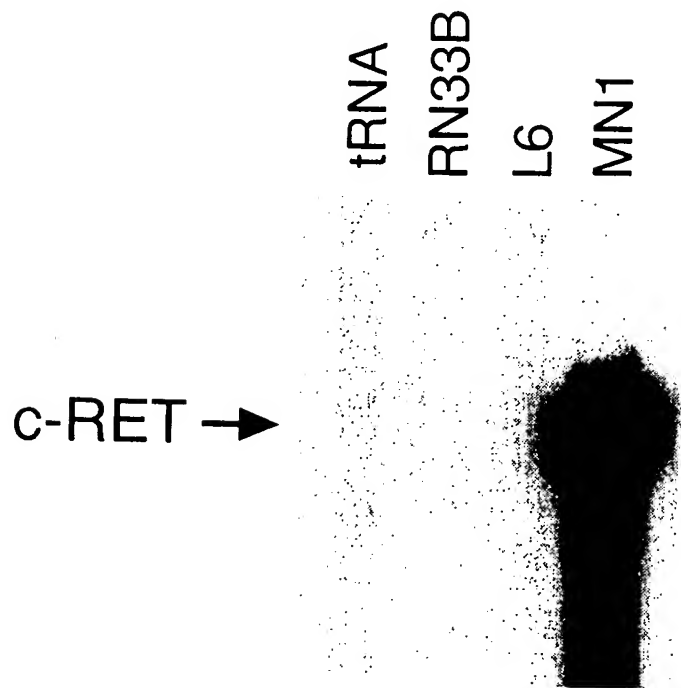
*FIG. 5A*



*FIG. 5B*

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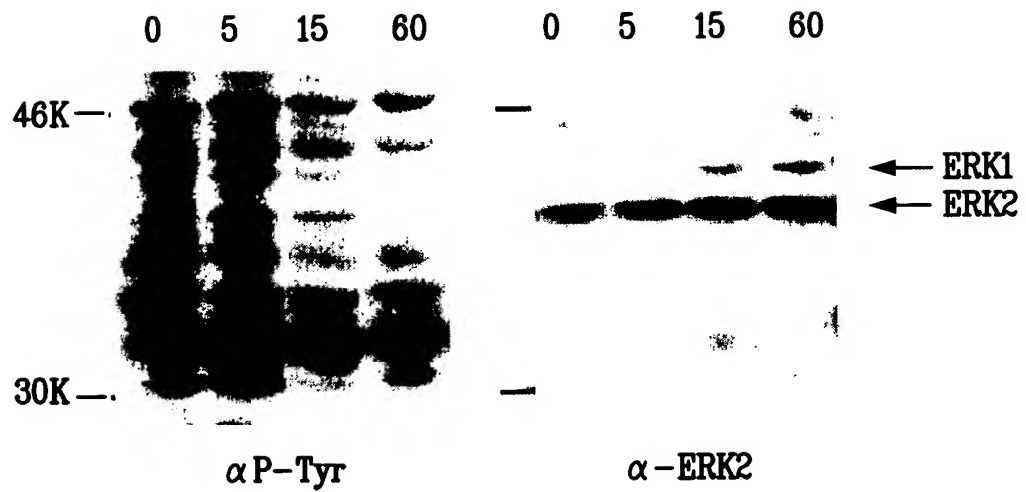
7



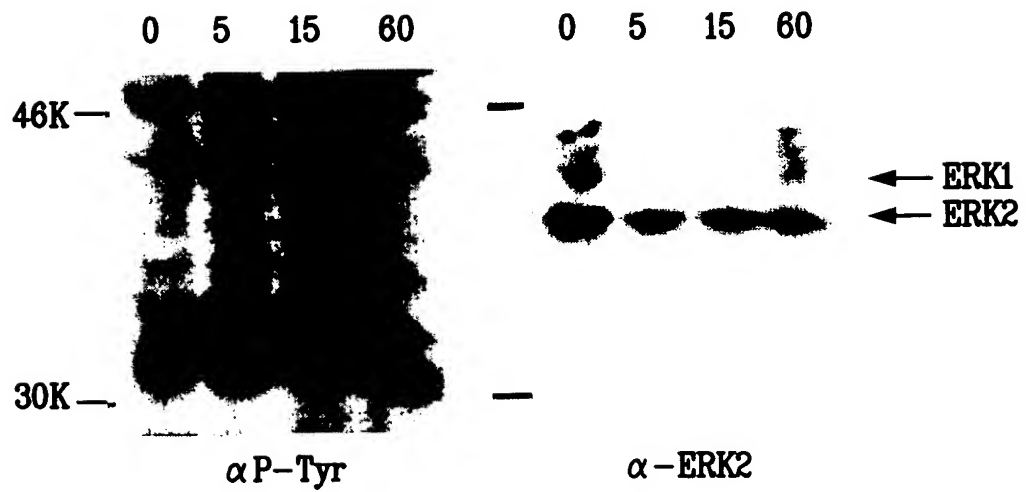
*FIG. 6*

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*FIG. 7A*

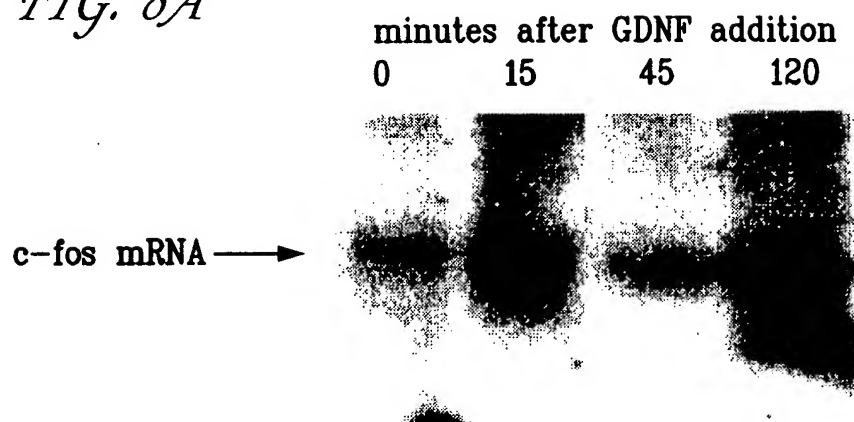


*FIG. 7B*

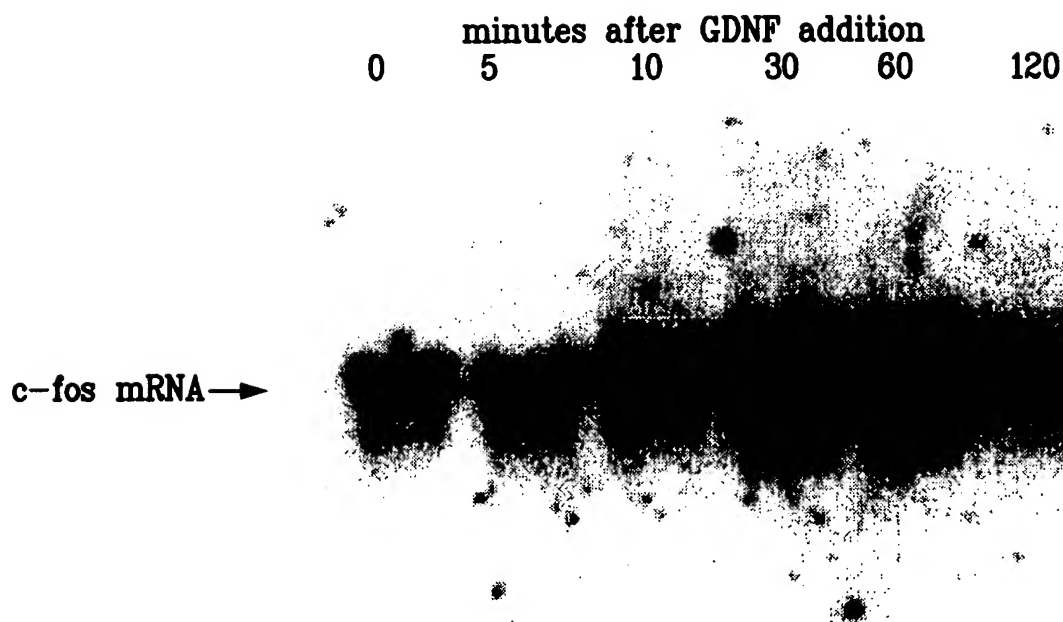


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*FIG. 8A*



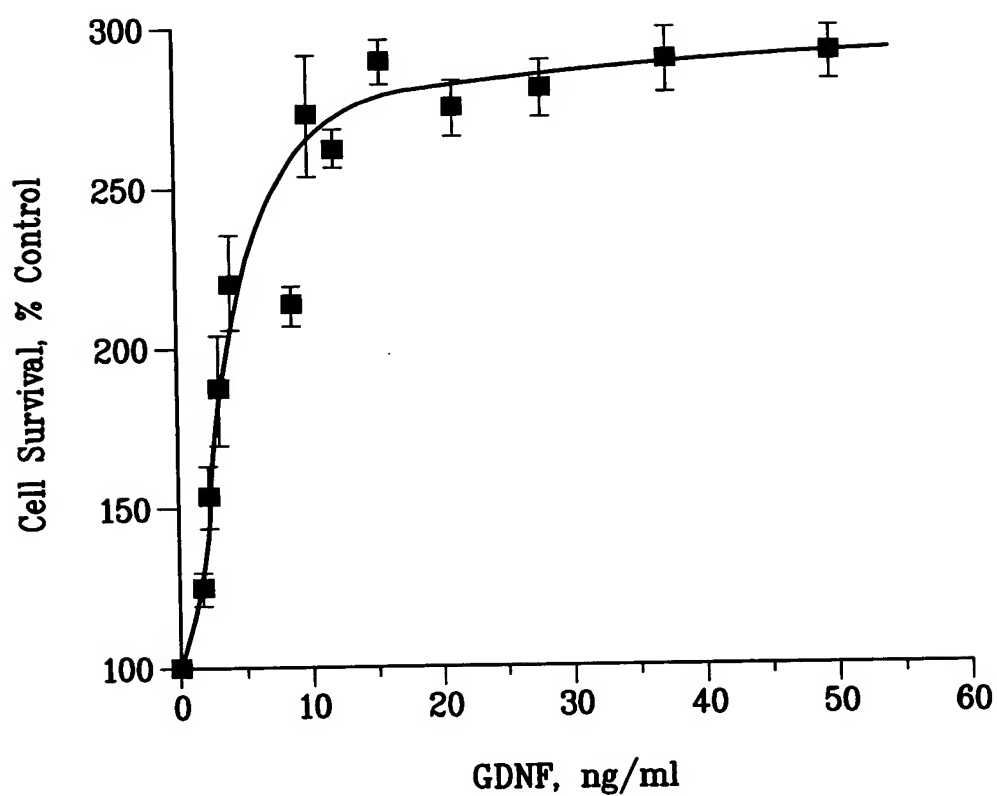
*FIG. 8B*



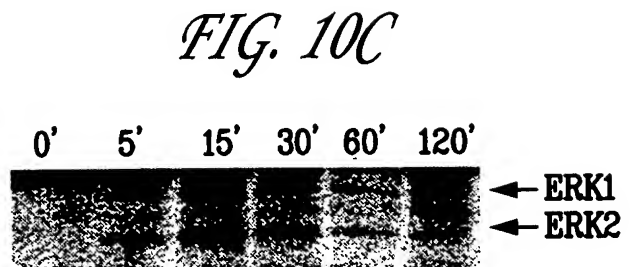
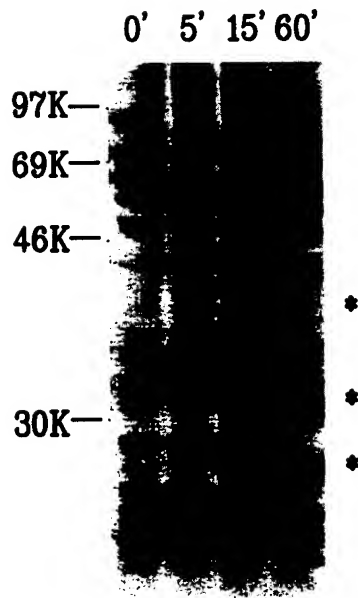
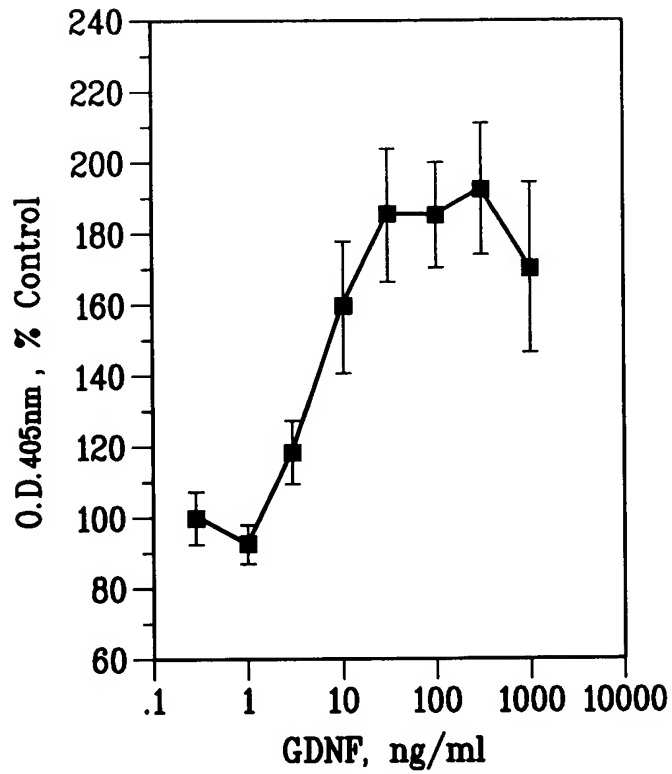


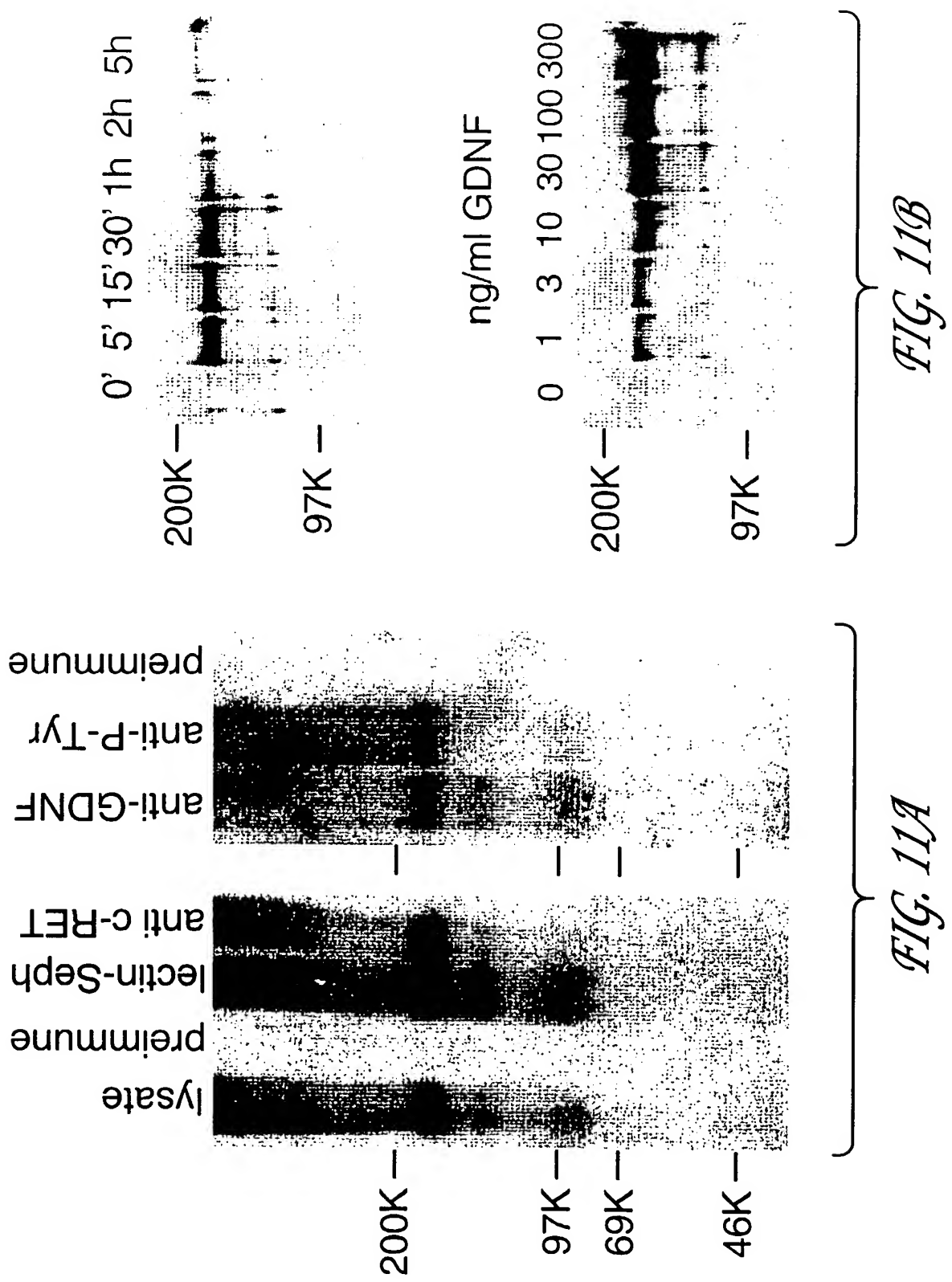
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*FIG. 9*

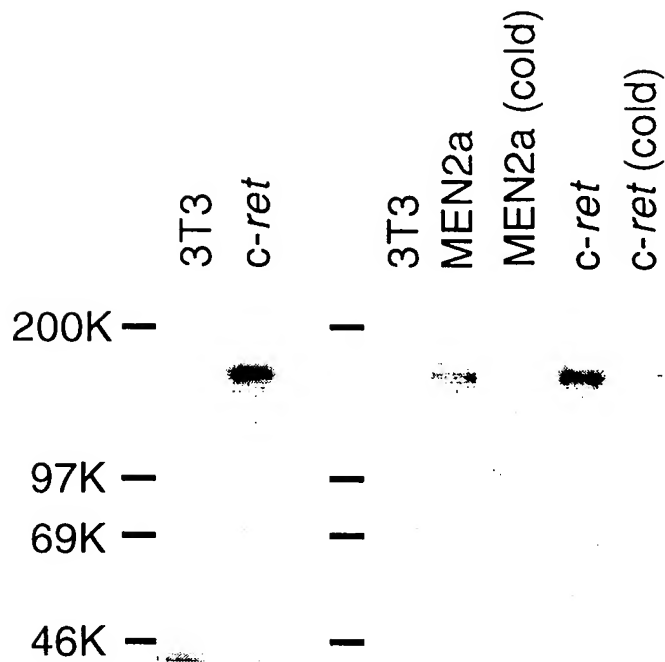


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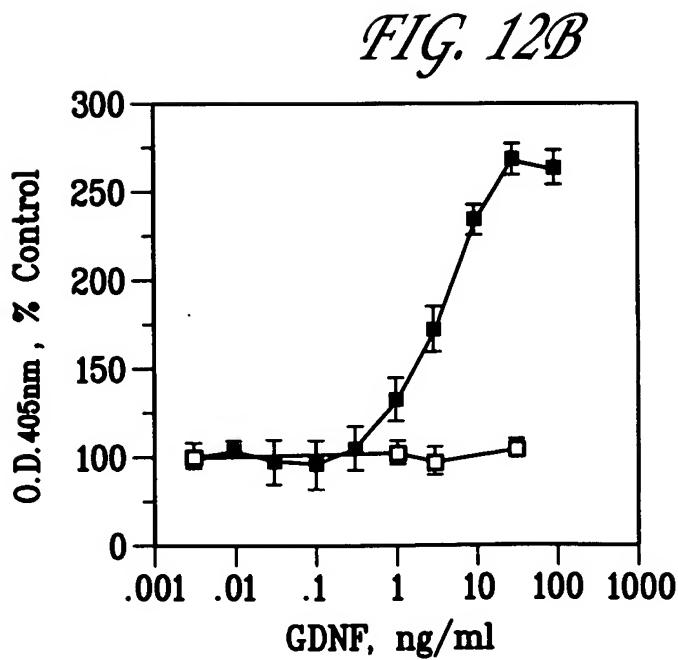




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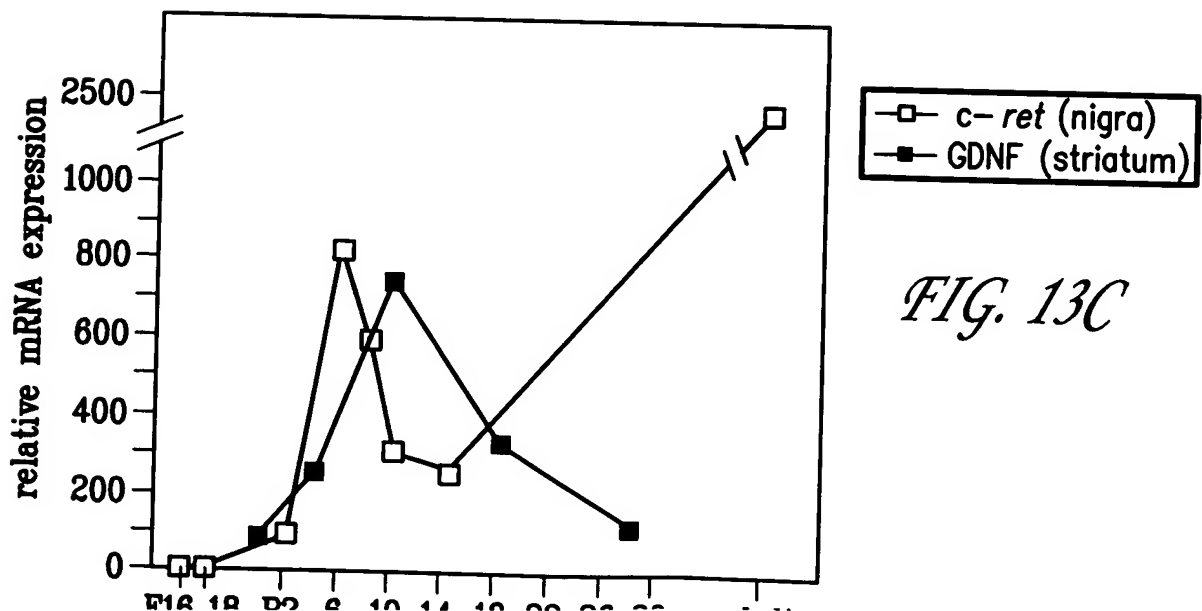
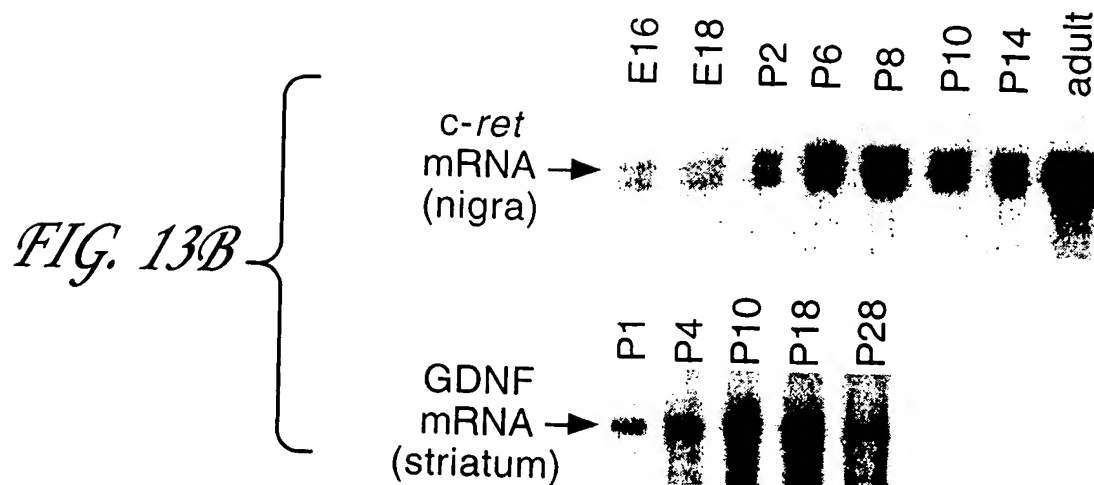
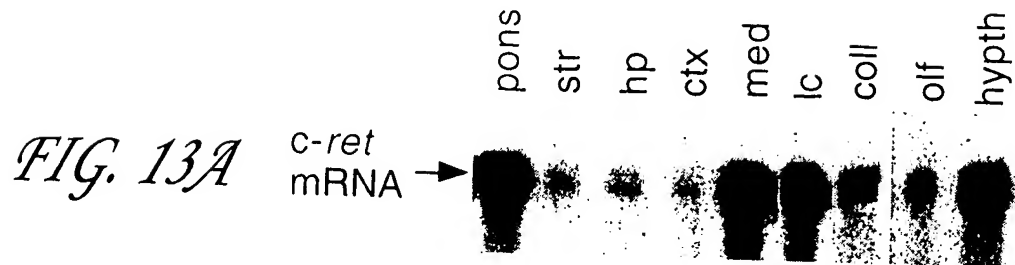


*FIG. 12A*



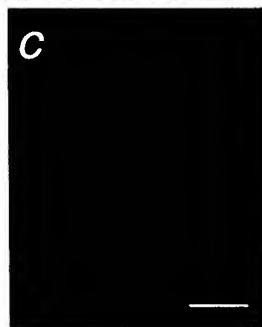
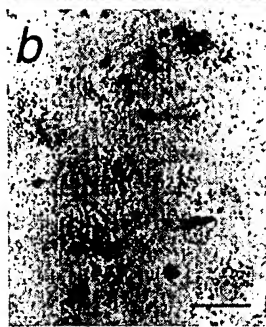
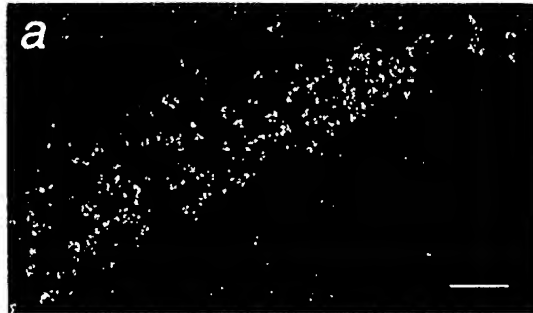
*FIG. 12B*

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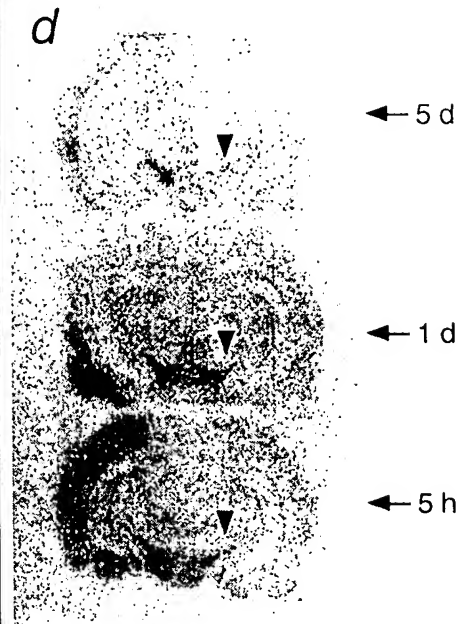


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*FIG. 14A*



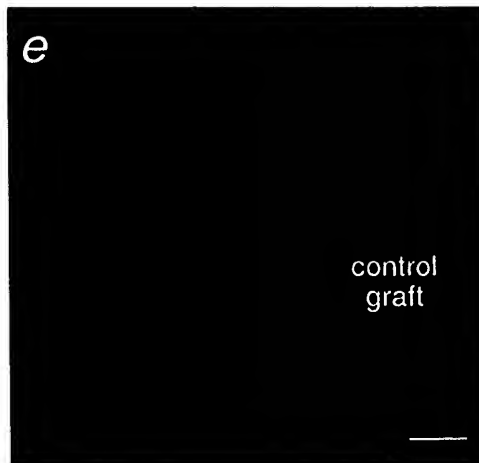
*FIG. 14D*



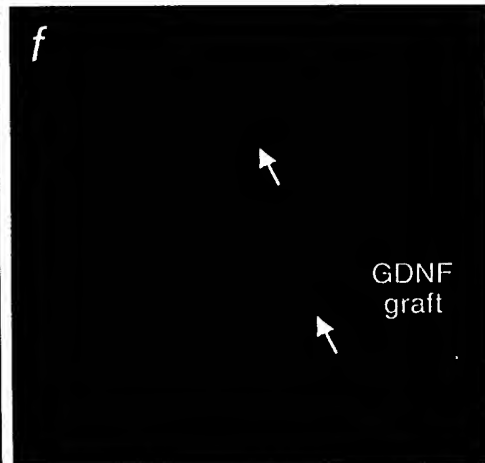
*FIG. 14B*

*FIG. 14C*

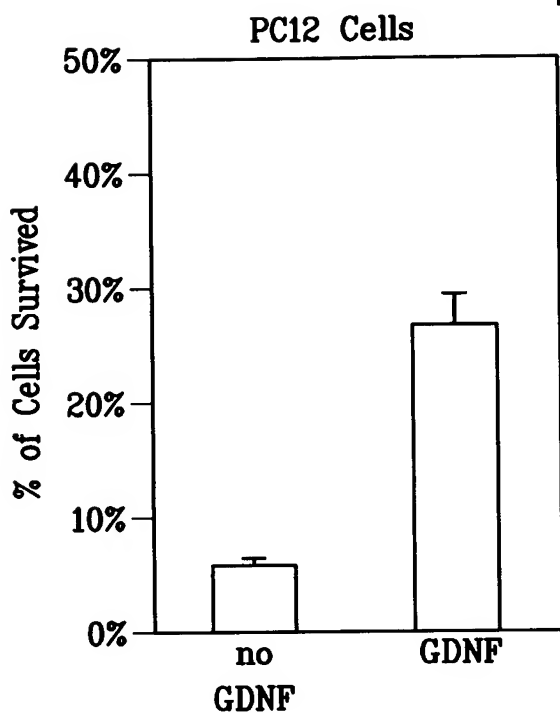
*FIG. 14E*



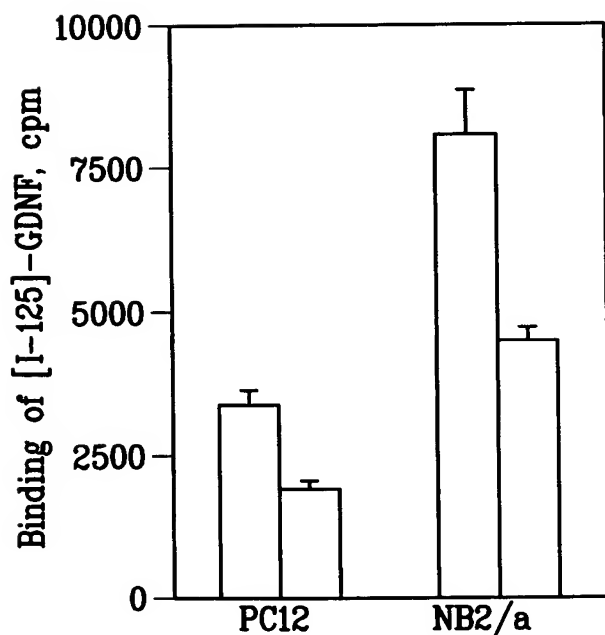
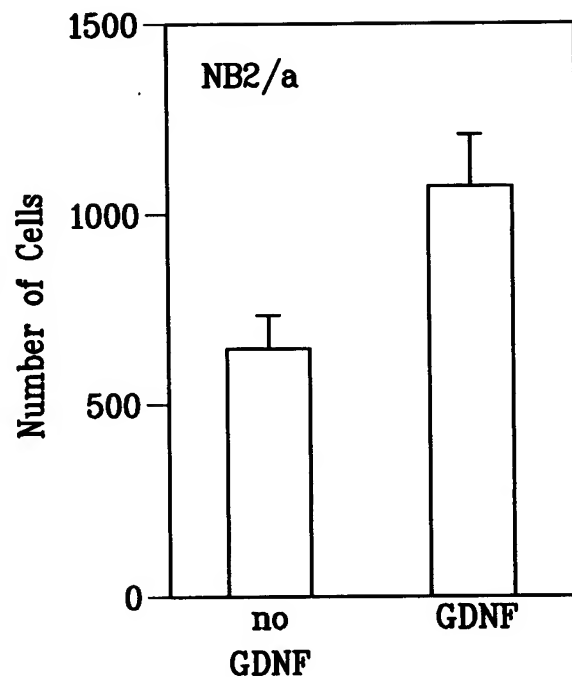
*FIG. 14F*



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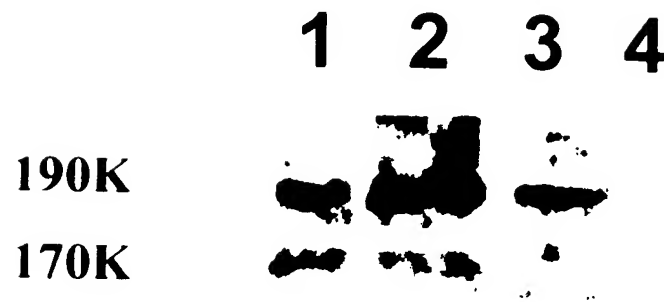


*FIG. 15A*



*FIG. 15C*

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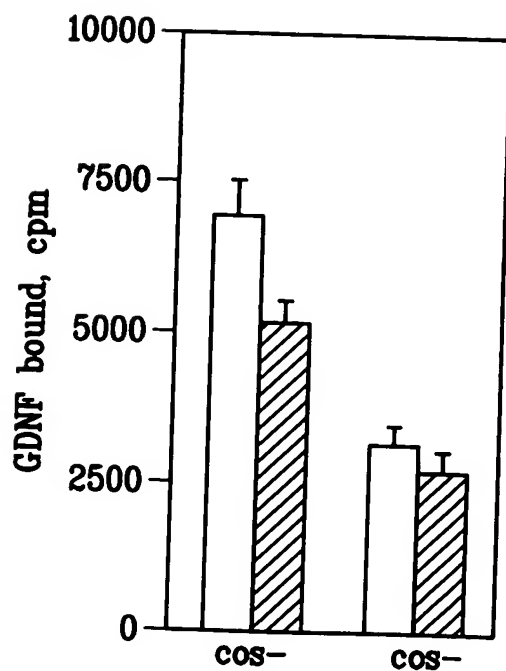
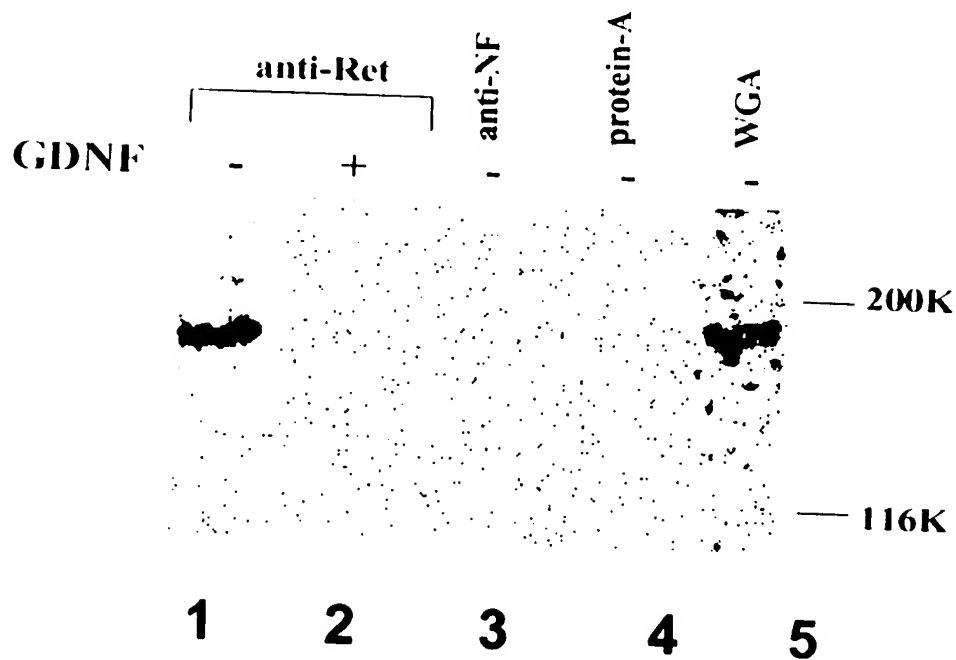


*FIG. 16*



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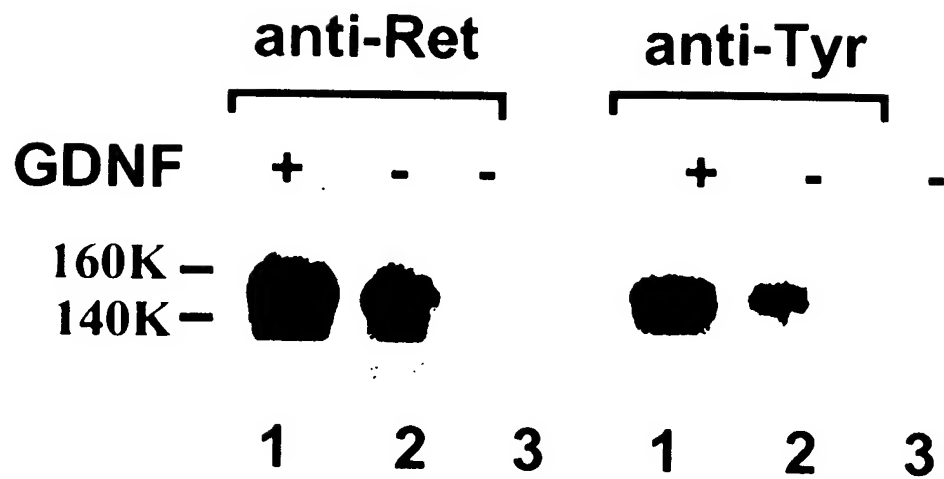
*FIG. 17A*



*FIG. 17B*

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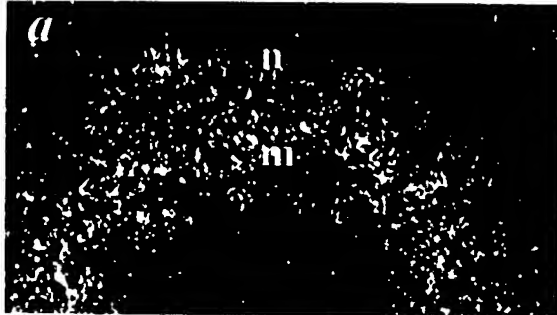
7



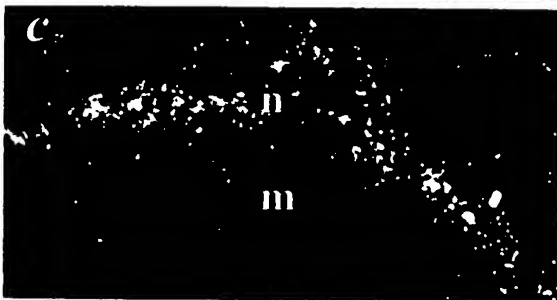
*FIG. 18*

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*FIG. 19A*



*FIG. 19B*

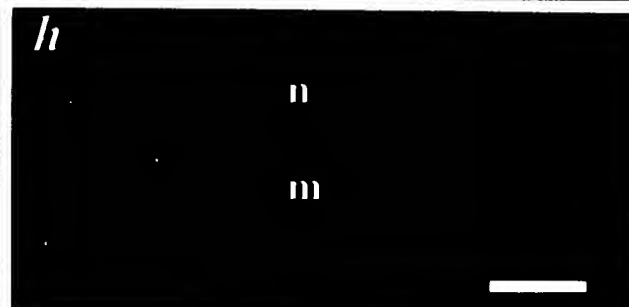
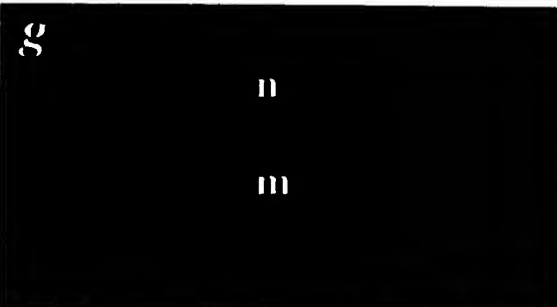
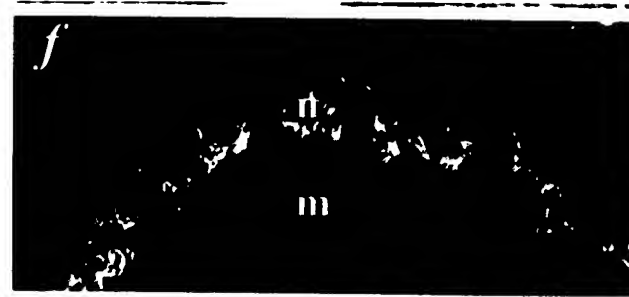
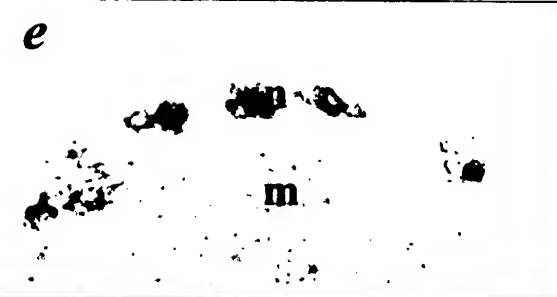


*FIG. 19C*

*FIG. 19D*

*FIG. 19E*

*FIG. 19F*

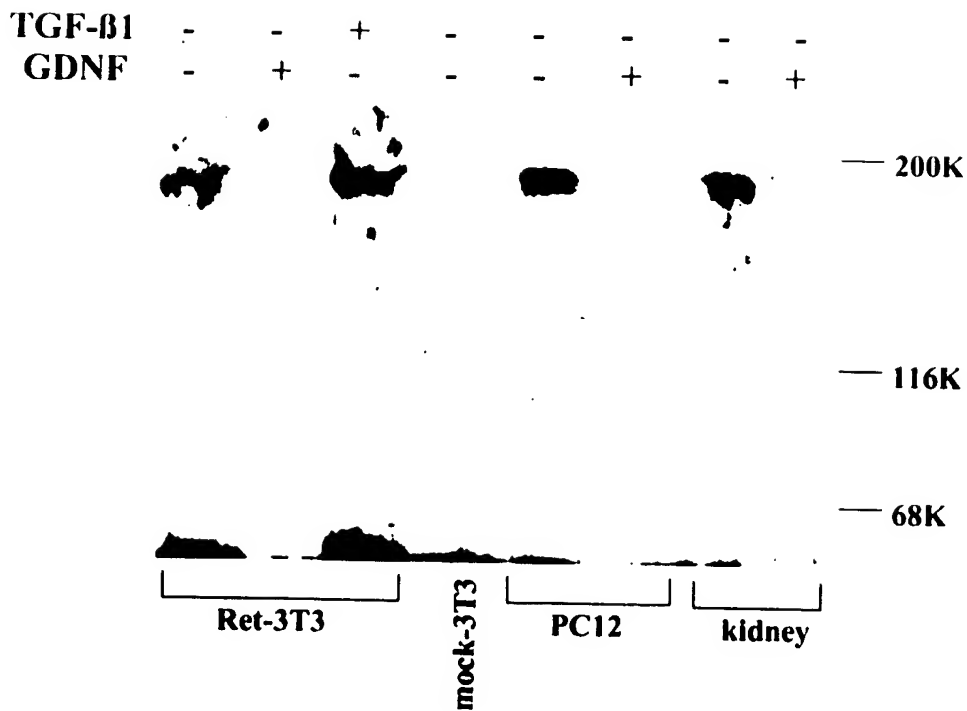
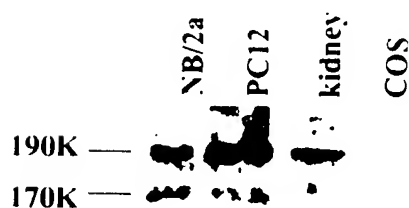


*FIG. 19G*

*FIG. 19H*

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*FIG. 20A*

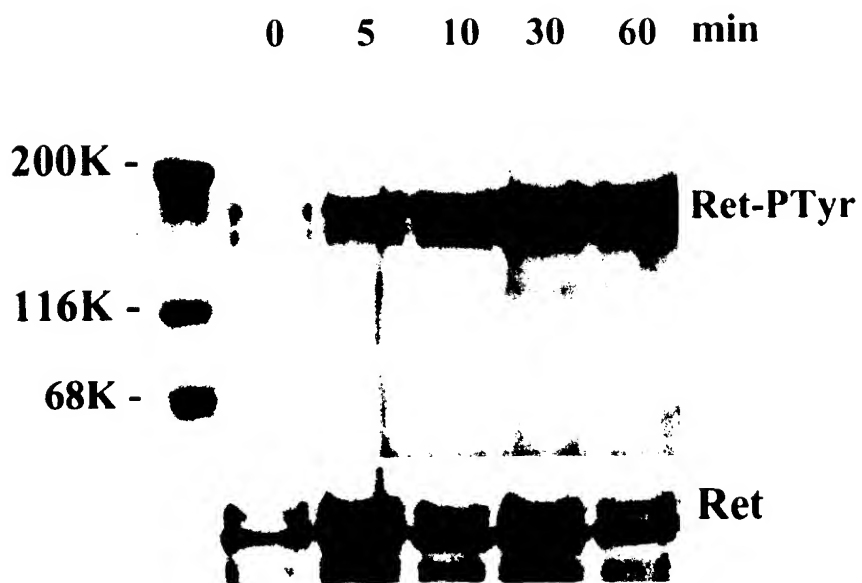
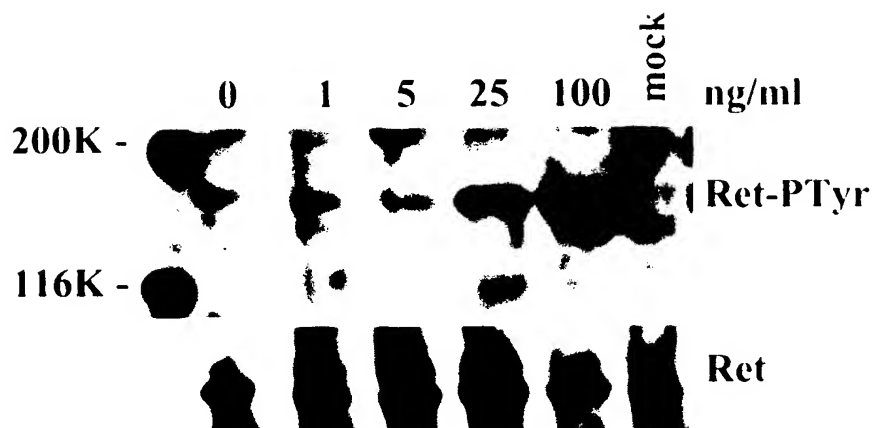


*FIG. 20B*

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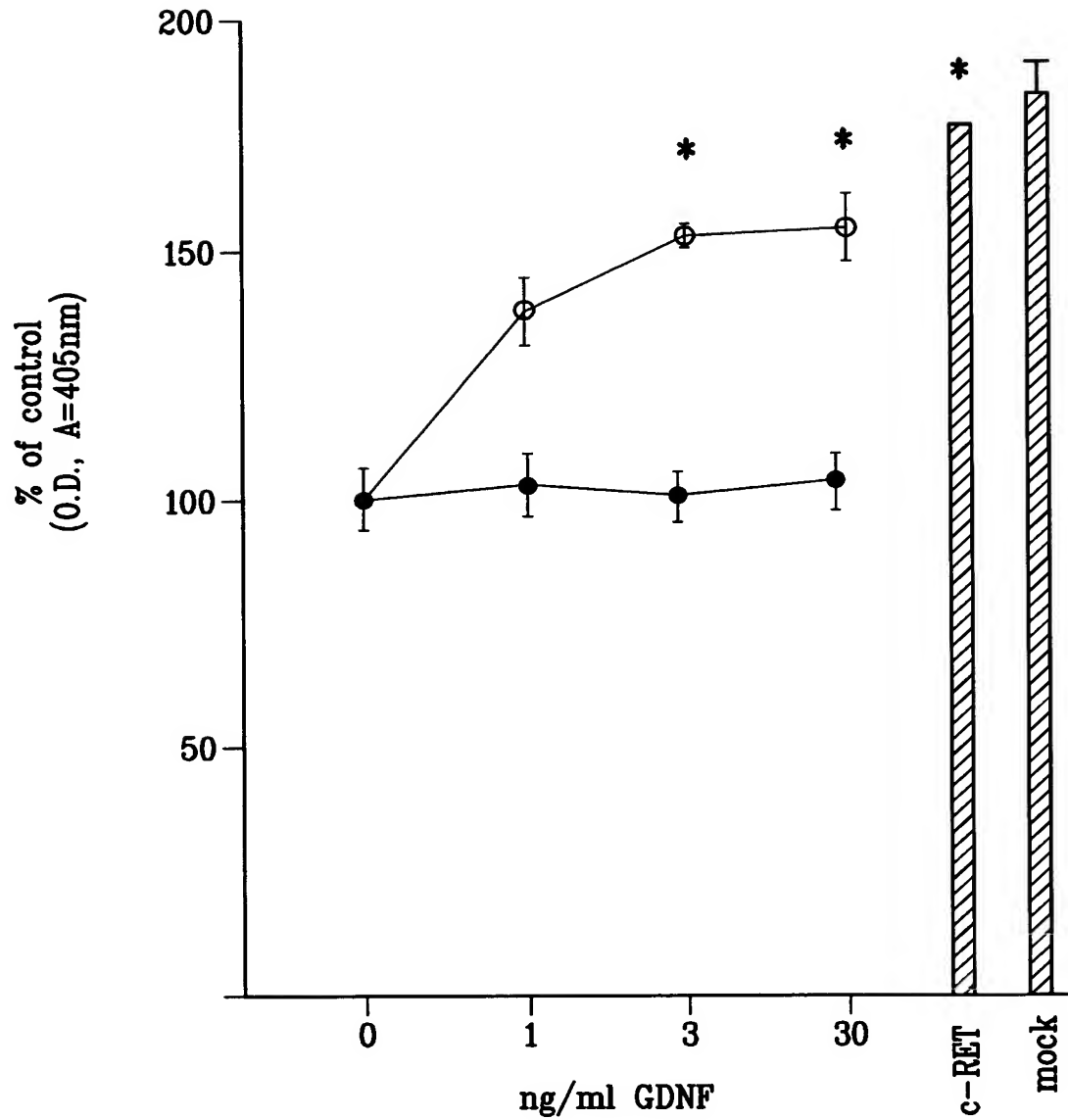
*FIG. 21A*



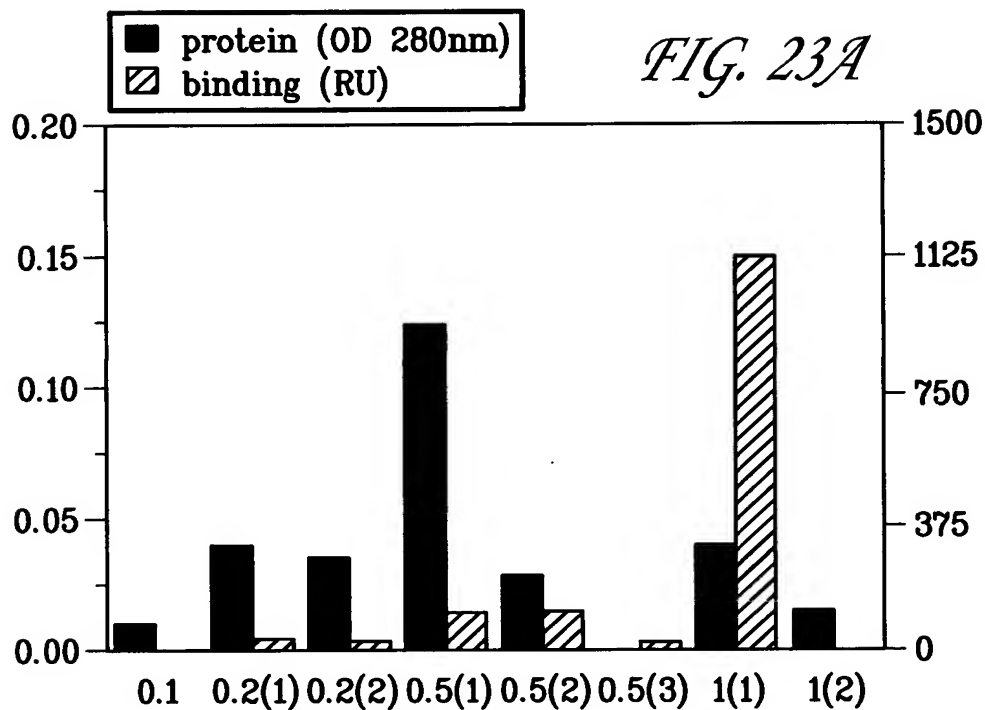
*FIG. 21B*

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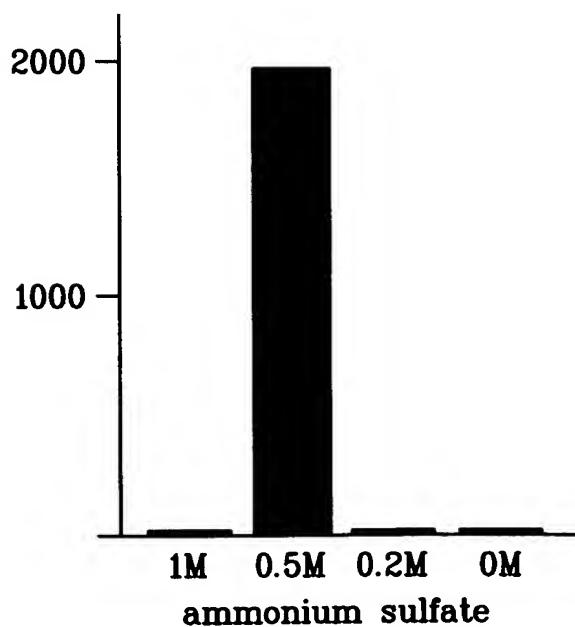
*FIG. 22*



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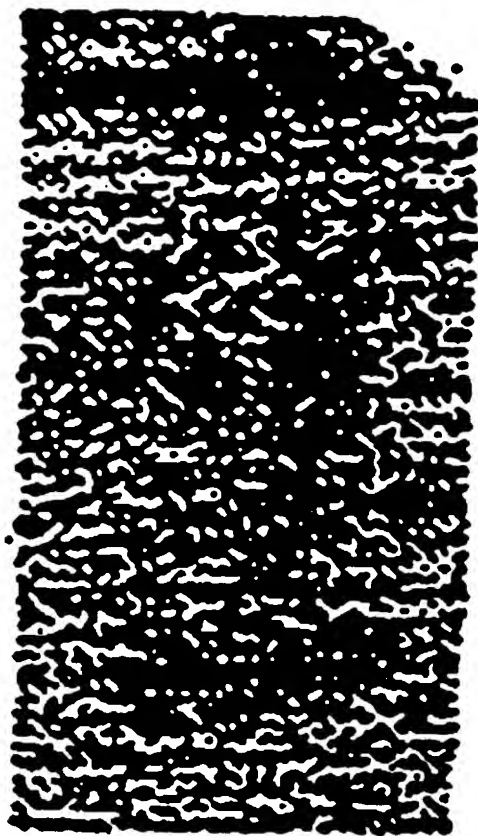


**FIG. 23B**



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3 2 1



*FIG. 24*

201 kD

117 kD

82 kD

47 kD

*FIG. 25*

1 MILANAFCLF FFLDETLRSL ASPSSLQGSE LHGWRPQVDC VRANELCAAE  
51 SNCSSRYRTL RQCLAGRDRN TMLANKECQA ALEVLQESPL YDCRCKRGMK  
101 KELQCLOIYW SIHLGLTEGE EFYEASPYEP VTSRLSDIFR LASIFSGTGT  
151 DPAVSTKSNH CLDAAKACNL NDNCKKLRS YISICNREIS PTERCNRRKC  
201 HKALRQFFDR VPSEYTYRML FCSCQDQACA ERRRQTILPS CSYEDKEKPN  
251 CLDLRSLCRT DHLCRSLAD FHANCRASYR TITSCPADNY QACLGSYAGM  
301 IGFDMPNYV DSNPTGIVVS PWCNCRGSGN MEECEKFLR DFTENPCLRN  
351 AIQAFNGTD VMSPKGPSL PATQAPRVEK TPSLPDDLSD STSLGTSVIT  
401 TCTSIQEQGL KANNSKELSM CFTELTTNIS PGSKKVIKLN SGSSRARLSA  
451 ALTALPLML TLAL SEQ ID NO:2



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GDNFR- $\beta$  1 MILANAFCLFFFLDETLRSLASPSSLQSELHGWRPQVDCVRANELCAAE 50  
|:| | . : : : | | : . . . | . : . : : | | : | : |  
GDNFR- $\alpha$  1 MFLATLYFALPLLDLLMSAEVSGD.....RLDCVKASDQCLKE 39  
  
51 SNCSSRYRTLROCLAGRDRN.....TMLANKECQAALBLQESPLYDCRC 95  
. | | . : | | | | | | : | | : : | : : | . . . | | : | | |  
40 QSCSTKYRTLROCVAGKETNFSLTSGLEAKDECRSAMEALKQKSLYNCR 89  
  
96 KRGMKKELQCLQIYWSYHLGLTEGEEFYEAAPYEPVTSRLSDIFRLASIF 145  
| | | | | | . | | . | | | : . : | : : : . | . | | | | | . | | | | | | : : :  
90 KRGMKKEKNCLRIYWSMYQSL.QGNDLLEDSPYEPVNSRLSDIFRAVPFI 138  
  
146 SGTGTDPAVSTKSNHCLDAAKACNLNDNCKKLRSSHISICNREISPTEC 195  
| : . : . . . | : | : | | | | | | | : | . | | . | | . | . : | . | |  
139 SDVFQQVEHISKGNCLDAAKACNLDDTCKKYRSAYITPCTTSM.S.NEVC 187  
  
196 NRRKCHKALRQFFDRVPSEYTYRMLFCSCQDQACAERRRQTILPSCSYED 245  
| | | | | | | | | | | : | | . . . | | | | | . | | . | | | | | : | | | :  
188 NRRKCHKALRQFFDKVPAKHSYGMLFCSCRDIACERRRQTIVPVCSYEE 237  
  
246 KEKPNCLDLRSLCRTDHLCSRSLADFHANCRASYRTITSCPADNYQACLG 295  
: | : | | | . | . . | : | : : : | | | | | | . | | : . | : . . . | : | | | |  
238 RERPNCLSLQDSCKTYNICRSLADFFTNCPESRSVSNCLKENYADCLL 287  
  
296 SYAGMIGFDMTPNYVDSNPTGIVVSPWCNCRGSGNMEEEECEKFLRDFTEN 345  
. | . | : | | | | | | | | | : : : | . | | | : | . | | | | | . | : |  
288 AYSGLIGTVMTPNYVDS..SSLSVAPWCDCSNSGNDLEDCLKFLNFFKTN 335  
  
346 PCLRNAIQAFNGGTDVNMSPKGPSLPATQAPRVEKTPSLPDDLSDSTS.. 393  
. | | : | | | | | | | | . | | . | . . . : | . . . | | . . . . . | : . . . |  
336 TCLKNAIQAFNGGSDVTMWQPAPPVQTTTATTTTAFRVKNKPLGPAGSEN 385  
  
394 .LGTSVITTCTSIQEQGLKAN..NSKELSMCFTELTTNISPGSKKVIKLN 440  
: . | | : . . | . . : | . | | | . | . | . | : : : : : : : : : | . . . | . .  
386 EIPTHVLPPCANLQAQKLKSNVSGSTHLCLSDSDFGKDGLAGASSHITTK 435  
  
441 SGSSRARLSAALTALPLIMLTAL\*..... 465 SEQ ID NO: 2  
| . | . | . . | | : | | | | |  
436 SMA..APPSCSLSSLPVLMILT.ALAALLSVSLEATS 468 SEQ ID NO: 1

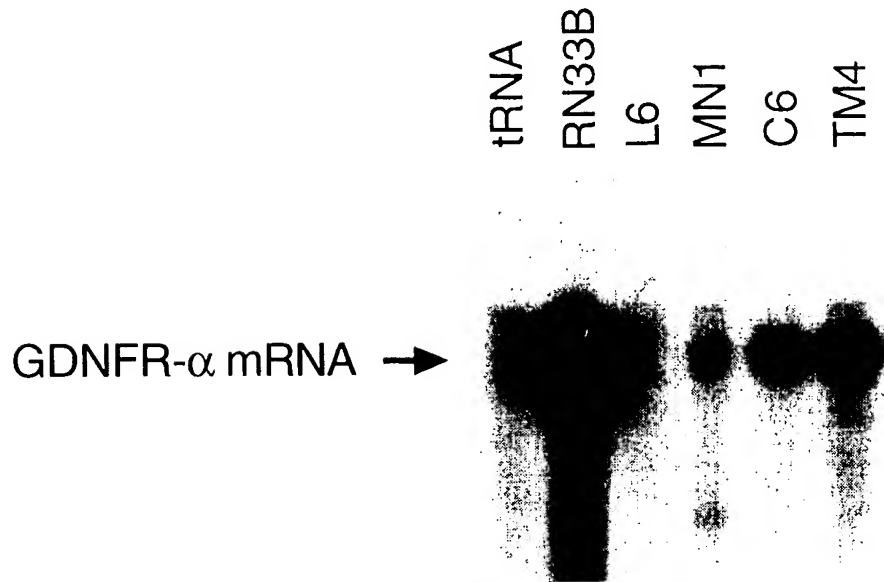
FIG. 26A

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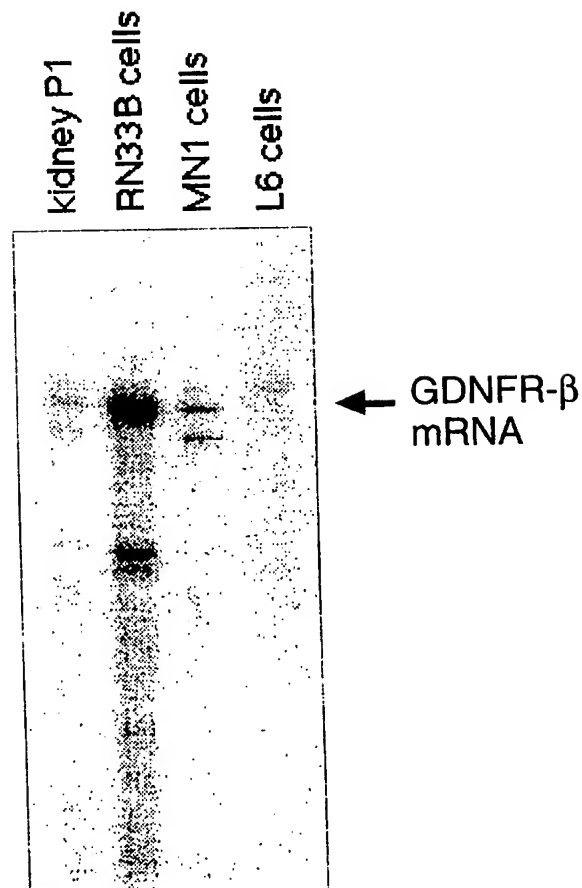
FIG. 26B

humalpa	MFLATLYFALPLDLLLSA.....EVSGGDRLLDCVKA	SDQCLKEQSCSKYRTLRCQVAGKETN	59
ratalpha	<u>MFLATLYFALPLDLLMSA.....EVSGGDRLLDCVKA</u>	<u>SDQCLKEQSCSKYRTLRCQVAGKETN</u>	59
ratbeta	MILANAFCLFFFLDFTLRSLASPSSLQGSSELHGWRPQVDCVRANELCAAESNCSSRYRTLRCQLAGRDRN		70
humbeta	<u>MILANAFCLFFFLDFTLRSLASPSSLQGPPELHGWRPPVDCVRANELCAAESNCSSRYRTLRCQLAGRDRN</u>		70
humalpa	FSLASGLEAKDECRSAMEALKQKSLYNCRCRKGKKEKNCRLIYWSMYQSL.QGNDLLEDSPYEPVNSRL		128
ratalpha	FSLTSGLEAKDECRSAMEALKQKSLYNCRCRKGKKEKNCRLIYWSMYQSL.QGNDLLEDSPYEPVNSRL		128
ratbeta	.....TMLANKECQAALEBLQESPLYDCRCRKGKKELOCLQIYWSYHLGLTEGEEFYEASPYEPVTSRL		135
humbeta	.....TMLANKECQAALEBLQESPLYDCRCRKGKKELOCLQIYWSYHLGLTEGEEFYEASPYEPVTSRL		135
humalpa	SDIFRVVPFISDVFOQVEHIPKGNNCILDAKACNLDDICKYRSAYITPCTTSVS.NDVNRRKCHKALR		198
ratalpha	SDIFRAVPFISDVFOQVEHISKGNNCILDAKACNLDDTCKYRSAYITPCTTSMS.NEVCNRRKCHKALR		198
ratbeta	SDIFRLASIFSGTGTDPAVSTKSNHCLDAKACNLNDNCKLRSSYISICNREISPTERCNRRKCHKALR		205
humbeta	SDIFRLASIFSGTGADPVVSAKSNHCLDAKACNLNDNCKLRSSYISICNREISPTERCNRRKCHKALR		205
humalpa	QFFDKVPAKHSYGMLEFCSCRDIACTERRRQTIIVPVCSEEREKPNCLSLQDSCKTNYICRSRLADFFTNC		268
ratalpha	QFFDKVPAKHSYGMLEFCSCRDIACTERRRQTIIVPVCSEEREKPNCLSLQDSCKTNYICRSRLADFFTNC		268
ratbeta	QFFDRVPSEYTYRMLFCSCQDQACAERRRQTIILPSCSYEDKEKPNCLDLRSLCRTDHLCRSRLADFHANC		275
humbeta	QFFDRVPSEYTYRMLFCSCQDQACAERRRQTIILPSCSYEDKEKPNCLDLRGVCRDTHLCRSRLADFHANC		275
humalpa	QPESRSVSSCLKENYADCLLAYSGLIGTVMTPNYIDSS..SLSVAPWPCDCNSGNDLEECCLKFLNFFKDN		336
ratalpha	QPESRSVSNCLKENYADCLLAYSGLIGTVMTPNYVDSS..SLSVAPWPCDCNSGNDLEDCCLKFLNFFKDN		336
ratbeta	RASYRTITSCPADNYQACLGSYAGMIGFDMTPNYVDNSNPTGIVVSPWCNCRGSGNMEEECEKFLRDFTEN		345
humbeta	RASYQTVTSCPADNYQACLGSYAGMIGFDMTPNYVDSSPTGIVVSPWCNCRGSGNMEEECEKFLRDFTEN		345
humalpa	TCLKNAIQAFNGSGDVTVMQPAFPVQTATA.TTTTALRVKNKPLGPAGSENEIPTHVLPPCANLQAOQLKS		406
ratalpha	TCLKNAIQAFNGSGDVTVMQPAFPVQTATA.TTTTAFRVKNKPLGPAGSENEIPTHVLPPCANLQAOQLKS		406
ratbeta	PCLRNAIQAFNGNGTDVNMSPKGPSPATQAPRVEKTPSLPDDLS DSTS...LGTSVITTTCTSIQEQGLKA		412
humbeta	<u>PCLRNAIQAFNGNGTDVNVSPKGPSPFQATQAPRVEKTPSLPDDLS DSTS...LGTSVITTTCTSVQEQGLKA</u>		412
humalpa	NVSGNTHLCISNGNYEKEGL.GASSHITTKSMA..APPSGGLSPLLVRVWTALSTLL..SLTETS*		465
ratalpha	<u>NVSGSTHLCILSDSDFGKDGLAGASSHITTKSMA..APPCSLSLPLVIMLTALAAALLSVSLEATS*</u>		465
ratbeta	<u>NNSKELSMCFTE..LTTNISP GSKVKIKLNSGSSL.....</u>		445
humbeta	<u>NNSKELSMCFTE..LTTNIIIPGSNKV IKPNSGSSRRARPSAALTVLSVIMLKQAL*</u>		464

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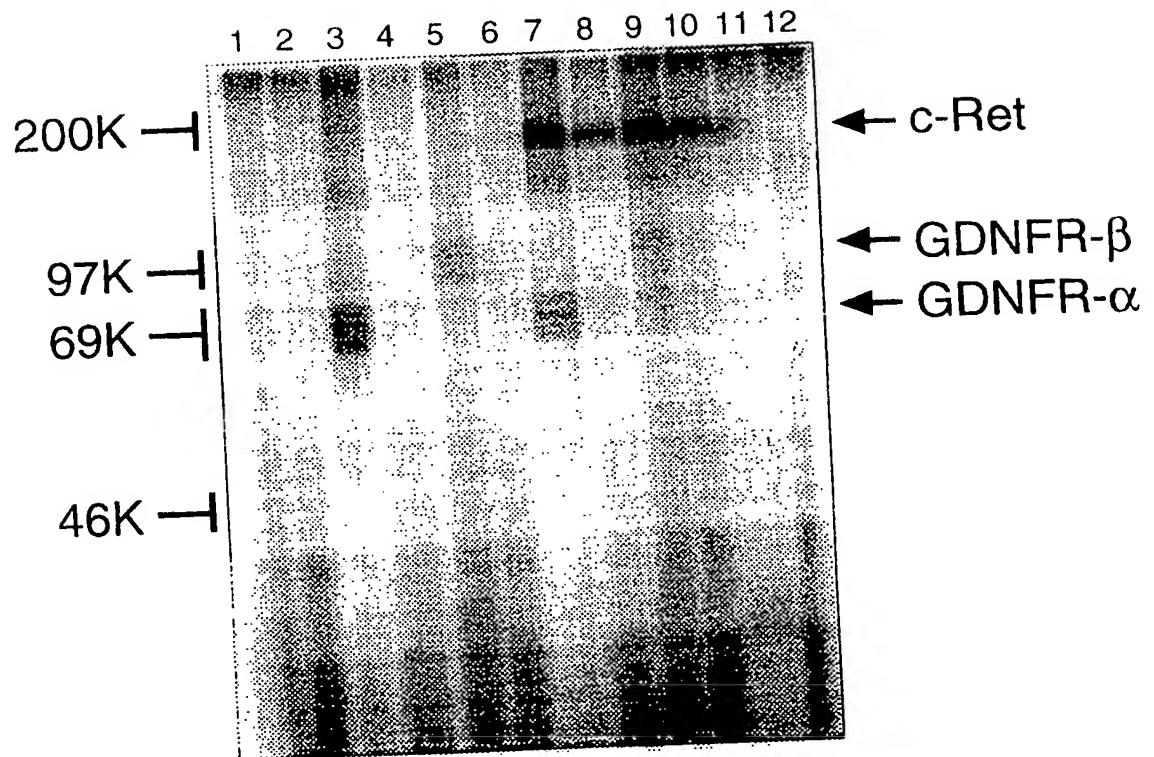
*FIG. 27*



*FIG. 28*

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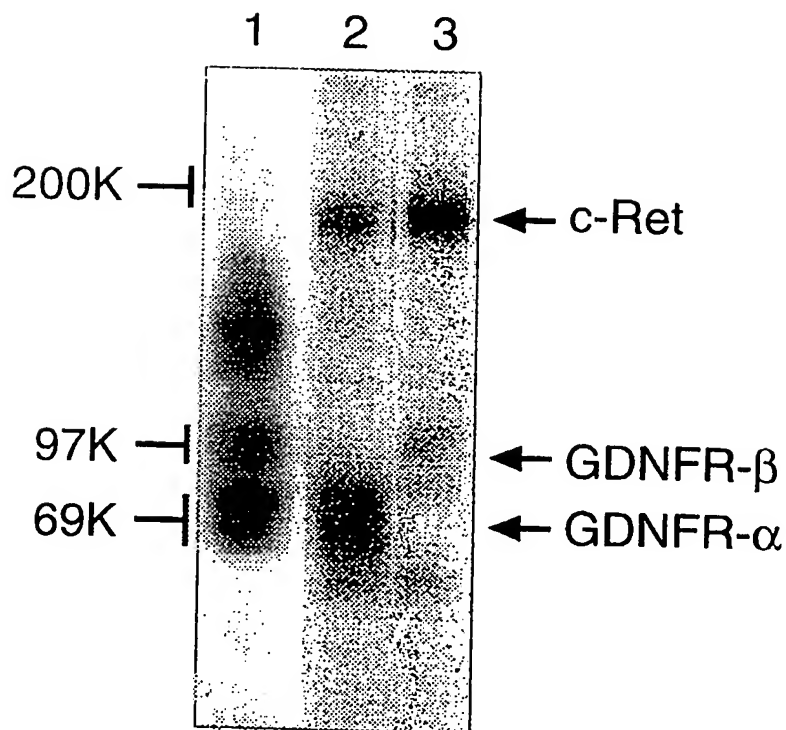
*FIG. 29*



- 1: control plasmid
- 2: control plasmid + cold
- 3: GDNFR- $\alpha$
- 4: GDNFR- $\alpha$  + cold
- 5: GDNFR- $\beta$
- 6: GDNFR- $\beta$  + cold
- 7: c-Ret + GDMFR- $\alpha$
- 8: c-Ret + GDMFR- $\alpha$  + cold
- 9: c-Ret + GDMFR- $\beta$
- 10: c-Ret + GDMFR- $\beta$  + cold
- 11: c-Ret
- 12: c-Ret + cold

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*FIG. 30*



1: RN33B

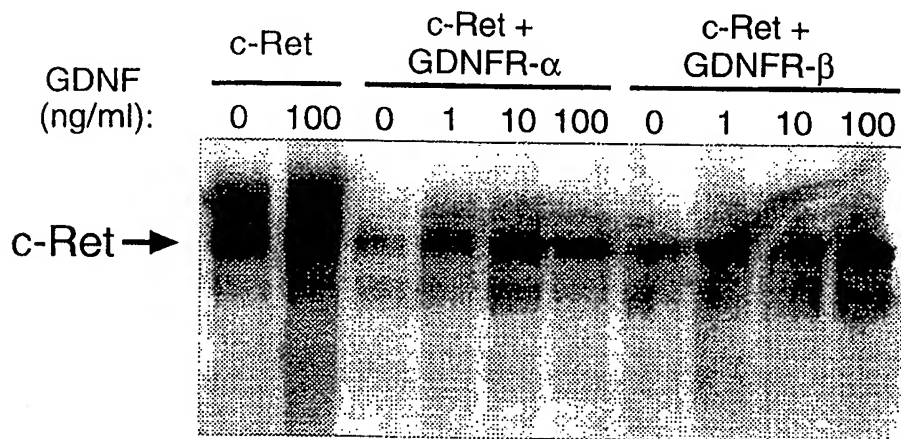
2: COS transfected with Ret and GDNFR- $\alpha$

3: COS transfected with Ret and GDNFR- $\beta$

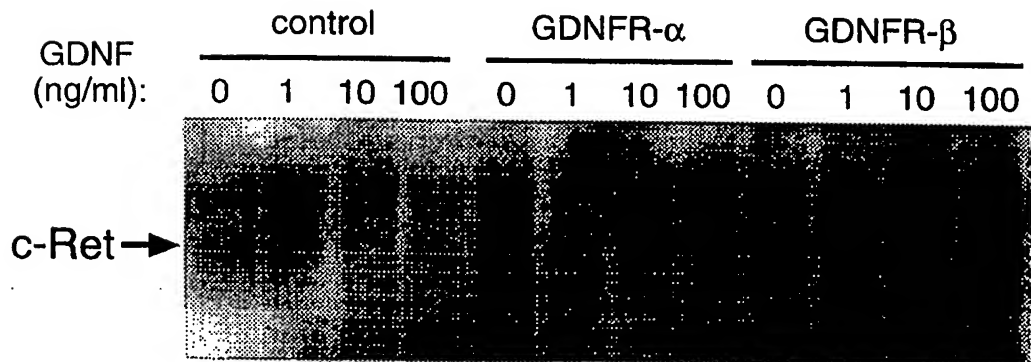
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# FIG. 31

COS cells transfected with c-Ret and GDNFR- $\alpha$  or GDNFR- $\beta$  cDNAs



Neuro-2A cells transfected with GDNFR- $\alpha$  or GDNFR- $\beta$  cDNAs



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*FIG. 32*

1 ATGATCTTGG CAAACGCCTT CTGCCTCTTC TTCTTTTGTAG ACGAAACCCCT  
51 CCGCTCTTTG GCCAGCCCTT CCTCCCTGCA GGGCTCTGAG CTCCACGGCT  
101 GGCGCCCCCA AGTGGACTGT GTCCGGGCCA ATGAGCTGTG TGGGGCTGAA  
151 TCCAACCTGCA GCTCCAGGTA CCGCACCCCTT CGGCAGTGCC TGGCAGGCCG  
201 GGATCGCAAT ACCATGCTGG CCAATAAGGA GTGCCAGGCA GCCCTGGAGG  
251 TCTTGCAGGA AAGCCCACTG TATGACTGCC GCTGCAAGCG GGGCATGAAG  
301 AAGGAGCTGC AGTGTCTGCA GATCTACTGG AGCATCCATC TGGGGCTGAC  
351 AGAGGGTGAG GAGTTCTATG AAGCTTCCCC CTATGAGCCT GTGACCTCGC  
401 GCCTCTCGGA CATCTTCAGG CTCGCTTCAA TCTTCTCAGG GACAGGGACA  
451 GACCCGGCAG TCAGTACCAA AAGCAACCAC TGCCTGGATG CCGCCAAGGC  
501 CTGCAACCTG AATGACAACCT GCAAGAAGCT TCGCTCCTCT TATATCTCCA  
551 TCTGCAACCG TGAGATCTCT CCCACCGAAC GCTGCAACCG CCGCAAGTGC  
601 CACAAGGCTC TGCGCCAGTT CTTTGACCGT GTGCCCAGCG AGTATACCTA  
651 CCGCATGCTC TTCTGCTCCT GTCAGGACCA GGCATGTGCT GAGCGTCGCC  
701 GGCAAACCAT CCTGCCCAGT TGCTCCTATG AGGACAAGGA GAAGCCCAAC  
751 TGCCTGGACC TGCGCAGCCT GTGTCGTACA GACCACCTGT GCCGGTCCCG  
801 ACTGGCAGAT TTCCACGCCA ACTGTCGAGC CTCCTACCGG ACAATCACCA  
851 GCTGTCCTGC GGACAACCTAC CAGGCATGTC TGGGCTCCTA TGCTGGCATG  
901 ATTGGGTTTG ATATGACACC CAACTATGTG GACTCCAACC CCACGGGCAT  
951 CGTGGTGTCT CCCTGGTGCA ATTGTCGTGG CAGTGGAAC ATGGAAGAAG  
1001 AGTGTGAGAA GTTCCTCAGG GACTTCACGG AAAACCCATG CCTCCGGAAT  
1051 GCCATTCAGG CCTTTGGTAA TGGCACAGAT GTGAACATGT CTCCCAAAGG  
1101 CCCCTCACTC CCAGCTACCC AGGCCCTCG GGTGGAGAAG ACTCCTTCAC  
1151 TGCCAGATGA CCTCAGTGAC AGCACCAGCC TGGGGACCAG TGTCATCACC  
1201 ACCTGCACAT CTATCCAGGA GCAAGGGCTG AAGGCCAACA ACTCCAAAGA  
1251 GTTAAGCATG TGCTTCACAG AGCTCACGAC AAACATCAGT CCAGGGAGTA  
1301 AAAAGGTGAT CAAACTTAAC TCAGGCTCCA GCAGAGCCAG ACTGTCTGGCT  
1351 GCCTTGACTG CCCTCCCACT CCTGATGCTG ACCTTGGCCT TGTAGGCCTT  
1401 TGAACCCAG CACA SEQ ID NO: 5

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5' **ATGATCTTGGCAACGCCCTTCTG**CCCTCTTCTTCTTTCTAGACGAGACCCCTCCGCTCTTTGGCCAGCCCTTCTCCTCCCTGCA 80  
GGCCCCGAGCTCCACGGCTGGCGCCCCCAGTGACTGTGTCCGGCCAAATGAGCTGTGTGCCGCCGAATCCAACTGCA 160  
GCTCTCGCTACCGCACTCTGCGCAGTGCCCTGGCAGGCCCGGACCGCAACACCATGCTGGCCAAACAAGGAGTGCCAGGCG 240  
GCCTTGGAGGCTTTGCAGGAGAGCCCCGCTGTACGACTGCCGCTGCAAGCGGGGCATGAAGAAGGAGCTGCAGTGTCTGGA 320  
GATCTACTGGAGCATCCACCTGGGGCTGACCGAGGGTGAGGAGTTCTACGAAGCCTCCCCCTATGAGCCGGTGACCTCCC 400  
GCCCTCGGACATCTTCAGGCTTGCTTCAATCTTCTCAGGGACAGGGGCAGACCCGGTGGTCAGCGCCAAAGAGCAACCAT 480  
TGCCTGGATGCTGCCAAGGCC**TGCAACCTGAATGACAACCTGCA**AAGAAGCTGCGCTCCTCCTACATCTC**CATCTGCA**ACCG 560  
CGAGATCTCGCCCAACGAGCGCTGCAACCGCCGCAAGTGCCACAAGGCCCTGGCCAGTTCTTCGACCCGGTGCCCAAGCG 640  
AGTACACCTACCGCATGCTCTTCTGCTCCTGCTGCCAAGACCAAGCGCTGCGCTGAGCGCCCGCGCAACCATCTCTGCCCAGC 720  
TGCTCCTATGAGGACAAGGAGAAGCCCCAAGTGCCTGGACCTGCGTGGCGTGTGCCGGACTGACCAACCTGTGTGGTCCCG 800  
GCTGGCCGACTTCCATGCCAATTGTCGAGCCTCCTACCAGACGGTCAACAGCTGCCCTGGGACAATTACCAGGCGTGTC 880  
TGGGCTCTTATGCTGGCATGATTGGGTTTGACATGACACCTAACTATGTGGACTCCAGCCCCACTGGCATCGTGGTGTCC 960  
CCCTGGTGCAGCTGTCTGTGGCAGCGGGAACATGGAGGAGGAGTGTGAGAAAGTTCTTCAGGGACTTCAACGAGAACCCATG 1040  
CCTCCGGAACGCCATCCAGGCCTTTGGCAACGGCACGGACGTGAACGTGTCCCCAAAGGCCCTCGTTCAGGGCCACCC 1120  
AGGCCCTCGGGTGGAGAAAGACGCCCTTCTTGGCAGATGACCTCAGTGACAGTACCAGCTTGGGACCCAGTGTATCACC 1200  
ACCTGCACGCTGTCTCCAGGACAGGGGCTGAAGGCCCAACAACCTCCAAAGAGTTAAGCATGTGCTTCAAGAGCTCACGAC 1280  
AAATATCATCCCAGGAGTAACAAGGTGATCAAACTTAAGTCAAGCCCCAGAGCCGAGACCGCTCGGCTGCCCTTGACCG 1360  
TGCTGTCTGTCTGATGCTGAACACAGGCCTT**TAG**GGCTGTGGGAACCGAGTCAGAAAGATTTTGAAACTACGCAGACAAG 1440  
AACAGCCGCCTGACGAAATGGAAACACACACAGACACACACCTTGC-3' 1490

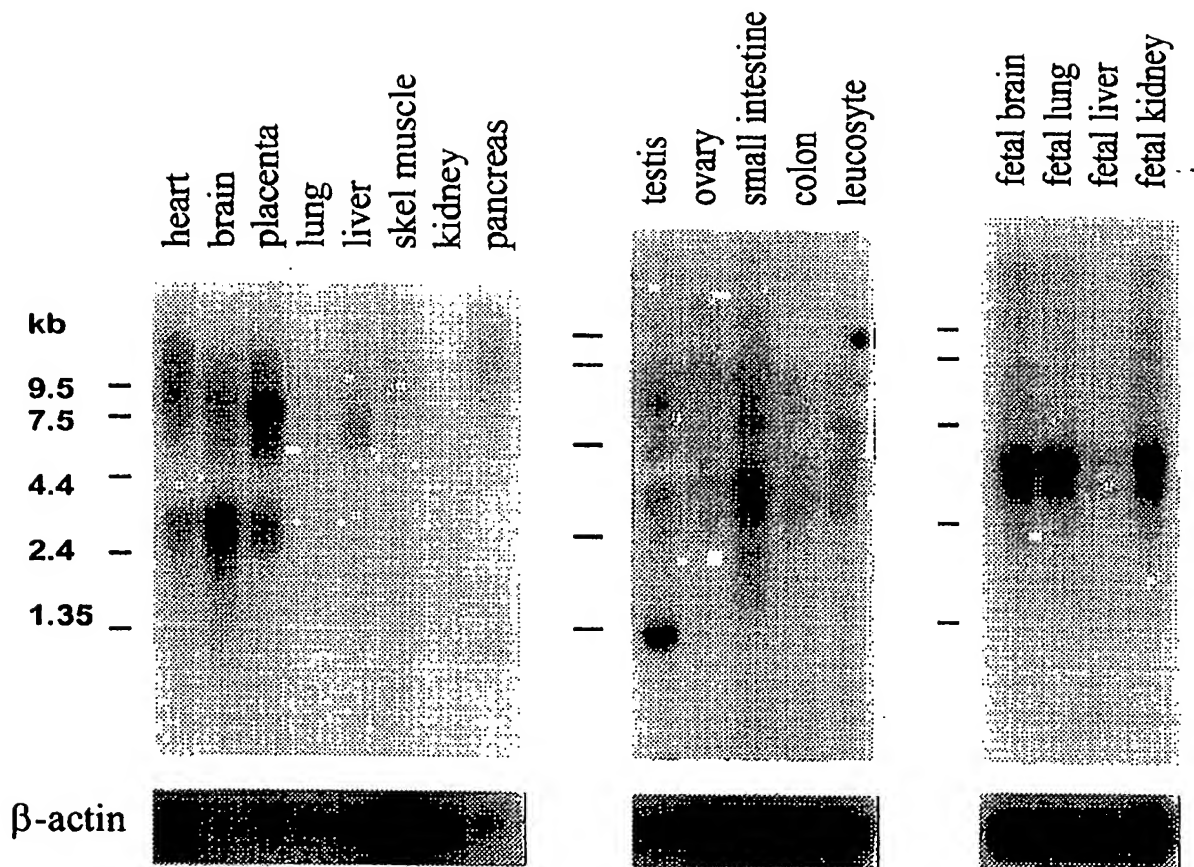
SEQ ID NO.:10

FIG. 33



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*FIG. 34*



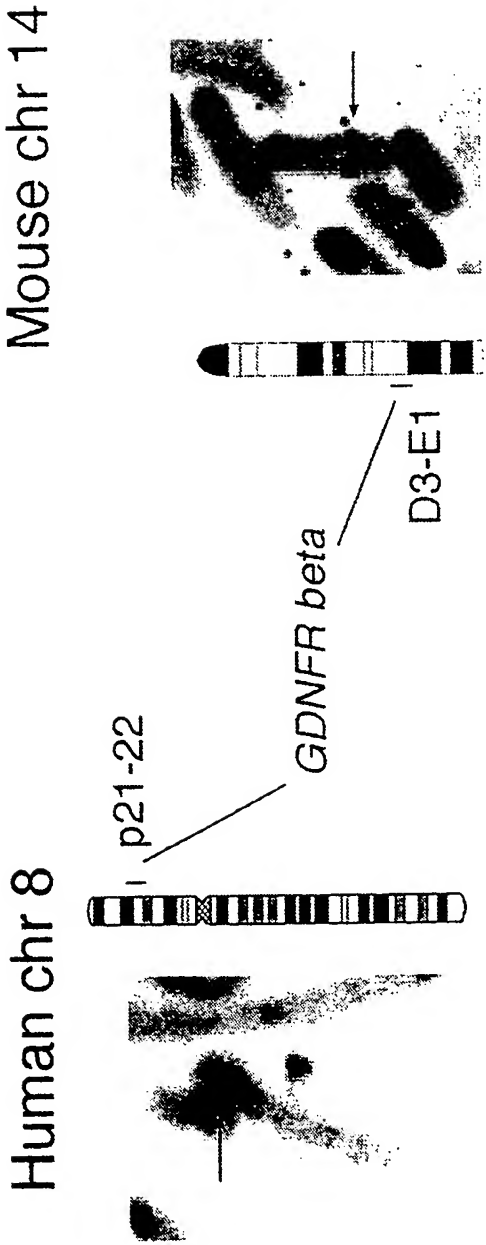




FIG. 37A



FIG. 37B



FIG. 37C



FIG. 37D



FIG. 37E

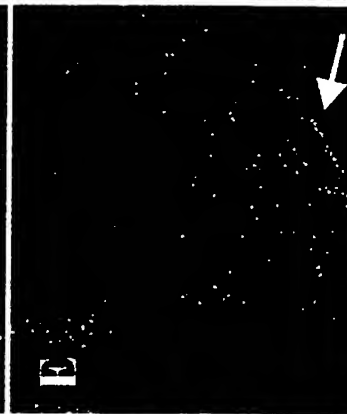


FIG. 37F



FIG. 37I

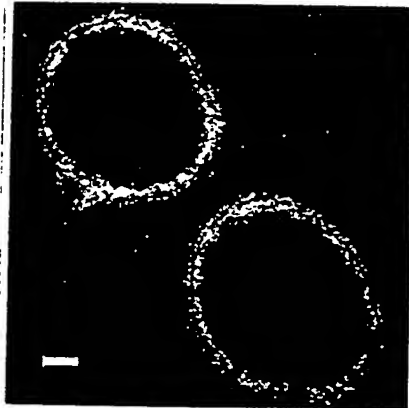


FIG. 37H

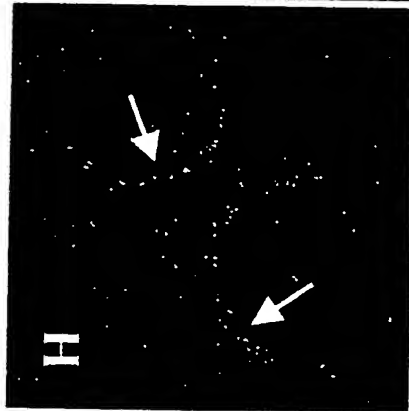


FIG. 37G

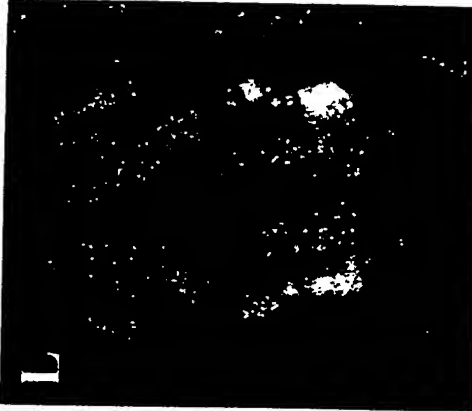


FIG. 37L

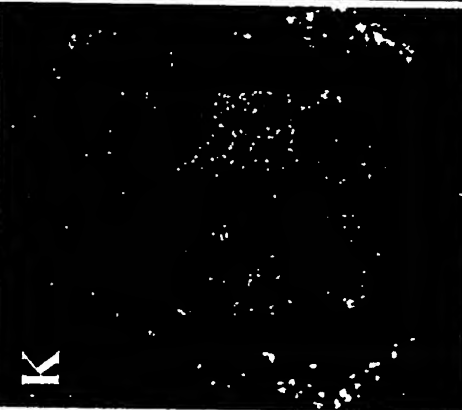


FIG. 37K



FIG. 37J

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*FIG. 37O*



*FIG. 37N*



*FIG. 37M*

